

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

(ii) TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and Uses Therefor

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Genentech, Inc.
- (B) STREET: 1 DNA Way
- (C) CITY: South San Francisco
- (D) STATE: California
- (E) COUNTRY: USA
- (F) ZIP: 94080

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE: 11-Jan-2000
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/899,437
- (B) FILING DATE: 07/24/1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Conley, Deirdre L.
- (B) REGISTRATION NUMBER: 36,487
- (C) REFERENCE/DOCKET NUMBER: P1084R1C1

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 650/225-2066
- (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2538 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: mouse NRG3 nucleic acid
- (B) LOCATION: 1-2538
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTGACCGGC CGGCGGCGCC CGGGCCGGTC TCGCCCCTCT ACCGAGCGCC 50  
TCGCCGCCCC CTCCCCGGCC CGCGTCCCCT CCCCCGTCCT CTCTCCCCG 100  
CCCGCCGCCC GCCTCTCGGG GGGAGGGGCG TGGGGGCAGG GAGCCGATTT 150  
GCATGCGGCC GCCGCGGCCG CTGCCTGAGC CGGAGCCCGC CGCCGCCGGA 200  
GCCCCGCCCC GCGCCCGCGC CCGGCCCGCG CGGCCCATG CCTCTGGCGC 250  
GGCCCTCGGG GGGGCGAAGG TGAAGATCGG CTCCTAGGAT GAGTGAAGGG 300  
GCGGCCGGTG CCTCGCCACC TGGTGCCGCT TCGGCAGCCG CCGCCTCAGC 350  
CGAGGAGGGC ACCGCGGCGG CTGCGGCGGC GCGGCGGGCG GCGGGGGGCC 400  
CGGACGGCGG CGGAGAAGGG GCGGCCGAAC CCCCCGGGA GTTACGCTGT 450  
AGCGACTGCA TCGTGTGGAA CCGGCAGCAG ACGTGGTTGT GCGTGGTGCC 500  
TCTGTTTCATC GGCTTCATCG GCCTGGGGCT CAGCCTCATG CTGCTTAAAT 550  
GGATCGTGGT AGGCTCCGTC AAGGAGTACG TGCCACGGA CCTGGTGGAC 600  
TCCAAGGGAA TGGGCCAGGA CCCCTTCTTC CTCTCCAAGC CCAGCTCTTT 650  
CCCCAAGGCT ATGGAAACCA CCACAACAAC CACTTCTACC ACGTCCCCCG 700  
CCACCCCTC TGCCGGCGGC GCCGCTTCTT CCAGGACGCC TAACCGGATT 750  
AGCACCCGCT TGACCACCAT CACACGGGCA CCCACCCGCT TCCCTGGGCA 800  
CCGGGTTCCC ATCCGGGCTA GCCGCGGCTC TACCACAGCA CGGAACACTG 850  
CTGCCCCTCC GACGGTCCTG TCCACCACGG CCCCTTCTT CAGTAGCAGC 900  
ACGCCCCGGT CCCGACCCC GATGCCAGGA GCCCCAGTA CGCAGGCGAT 950  
GCCTTCCTGG CCCACTGCGG CGTATGCTAC CTCCTCCTAC CTCCACGATT 1000  
CCACTCCCTC CTGGACCCTG TCACCCTTTC AGGATGCTGC TGCCGCCTCT 1050  
TCCTCCTCAC CCTCTTCCAC CTCCTCCACT ACCACCACCC CAGAAACTAG 1100  
CACCAGCCCC AAATTTTATA CTACAACATA CTCCACTGAA CGATCTGAGC 1150  
ACTTCAAACC CTGTCGAGAC AAGGACCTGG CGTATTGTCT CAATGATGGT 1200  
GAATGCTTTG TGATTGAGAC CCTGACAGGA TCCATAAGC ACTGTCGGTG 1250  
CAAGGAAGGC TACCAAGGAG TCCGTTGTGA TCAATTTCTG CCGAAAACAG 1300  
ACTCCATCTT ATCGGATCCA ACAGACCACT TGGGGATTGA ATTCATGGAG 1350  
AGTGAAGACG TTTATCAAAG GCAGGTGCTG TCAATTTTAT GTATCATCTT 1400

TGGAATTGTC ATCGTGGGCA TGTTCGTGTC AGCATTCTAC TTCAAAAGCA 1450  
 AGAAACAAGC TAAACAAATT CAGGAGCACC TGAAAGAGTC ACAGAATGGG 1500  
 AAGAACTACA GCCTCAAGGC ATCCAGCACA AAGTCTGAGA GCTTGATGAA 1550  
 GAGCCATGTC CATCTACAAA ATTATTCAAA GGCGGATAGG CATCCTGTGA 1600  
 CTGCGCTGGA GAAAATAATG GAGTCAAGTT TTTCAGCTCC CCAGTCGTTC 1650  
 CCAGAAGTCA CTTCTCCTGA CCGAGGAAGC CAGCCTATCA AGCACCACAG 1700  
 CCCAGGACAA AGGAGTGGGA TGTTCGCATAG GAATACTTTC AGAAGGGCAC 1750  
 CACCCTCACC CCGAAGTCGA CTGGGTGGTA TTGTAGGACC AGCATATCAA 1800  
 CAACTTGAAG AATCAAGAAT TCCAGACCAG GATACGATAC CTTGCCAAGG 1850  
 GATAGAGGTC AGGAAGACTA TATCCCACCT GCCTATACAG CTGTGGTGTG 1900  
 TTGAAAGACC CCTGGACTTA AAGTATGTGT CCAATGGCTT AAGAACCCAA 1950  
 CAAATGCAT CAATAAATAT GCAACTGCCT TCAAGAGAGA CAAACCCCTA 2000  
 TTTTAATAGC TTGGATCAAA AGGACCTGGT GGGTTATTTA TCCCCAAGGG 2050  
 CCAATTCTGT GCCATCATC CCGTCGATGG GTCTAGAAGA AACCTGCATG 2100  
 CAAATGCCAG GGATTTCTGA CGTCAAAAGC ATTAAATGGT GCAAAAACTC 2150  
 CTACTCCGCT GACATTGTCA ACGCGAGTAT GCCAGTCAGT GATTGTCTTC 2200  
 TAGAAGAACA ACAGGAAGTG AAAATATTAC TAGAGACTGT GCAGGAACAG 2250  
 ATCCGGATTC TGA CTGATGC CAGACGGTCA GAAGACTTCG AACTGGCCAG 2300  
 CATGGAACT GAGGACAGTG CGAGCGAAAA CACAGCCTTT CTCCCCCTGA 2350  
 GTCCACGGC CAAATCAGAA CGAGAGGCAC AATTTGTCTT AAGAAATGAA 2400  
 ATACAAAGAG ACTCTGTGCT AACCAAGTGA CTGGAAATGT AGGAATCTGT 2450  
 GCATTATATG CTTTGCTAAA CAGGAAGGAG AGGAAATTAA ATACAAATTA 2500  
 TTTATATGCA TTAATTTAAG AGCATCTACT TAGAAGCC 2538

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.
- (B) LOCATION: 1-713
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Glu	Gly	Ala	Ala	Gly	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	
1				5					10					15	
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	
				20					25					30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	
				35					40					45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	
				50					55					60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	
				65					70					75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	
				80					85					90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	
				95					100					105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	
				110					115					120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	
				125					130					135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	
				140					145					150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	
				155					160					165	
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	
				170					175					180	
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Pro	Thr	Val	Leu	Ser	
				185					190					195	
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Pro	Gly	Ser	Arg	Pro	
				200					205					210	
Pro	Met	Pro	Gly	Ala	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro	
				215					220					225	
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro	
				230					235					240	
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ala	Ala	Ser	Ser	
				245					250					255	
Ser	Ser	Pro	Ser	Ser	Thr	Ser	Ser	Thr	Thr	Thr	Thr	Pro	Glu	Thr	
				260					265					270	
Ser	Thr	Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	
				275					280					285	

Ser	Glu	His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	290	295	300
Leu	Asn	Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	305	310	315
His	Lys	His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	320	325	330
Asp	Gln	Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	335	340	345
Asp	His	Leu	Gly	Ile	Glu	Phe	Met	Glu	Ser	Glu	Asp	Val	Tyr	Gln	350	355	360
Arg	Gln	Val	Leu	Ser	Ile	Ser	Cys	Ile	Ile	Phe	Gly	Ile	Val	Ile	365	370	375
Val	Gly	Met	Phe	Cys	Ala	Ala	Phe	Tyr	Phe	Lys	Ser	Lys	Lys	Gln	380	385	390
Ala	Lys	Gln	Ile	Gln	Glu	His	Leu	Lys	Glu	Ser	Gln	Asn	Gly	Lys	395	400	405
Asn	Tyr	Ser	Leu	Lys	Ala	Ser	Ser	Thr	Lys	Ser	Glu	Ser	Leu	Met	410	415	420
Lys	Ser	His	Val	His	Leu	Gln	Asn	Tyr	Ser	Lys	Ala	Asp	Arg	His	425	430	435
Pro	Val	Thr	Ala	Leu	Glu	Lys	Ile	Met	Glu	Ser	Ser	Phe	Ser	Ala	440	445	450
Pro	Gln	Ser	Phe	Pro	Glu	Val	Thr	Ser	Pro	Asp	Arg	Gly	Ser	Gln	455	460	465
Pro	Ile	Lys	His	His	Ser	Pro	Gly	Gln	Arg	Ser	Gly	Met	Leu	His	470	475	480
Arg	Asn	Thr	Phe	Arg	Arg	Ala	Pro	Pro	Ser	Pro	Arg	Ser	Arg	Leu	485	490	495
Gly	Gly	Ile	Val	Gly	Pro	Ala	Tyr	Gln	Gln	Leu	Glu	Glu	Ser	Arg	500	505	510
Ile	Pro	Asp	Gln	Asp	Thr	Ile	Pro	Cys	Gln	Gly	Ile	Glu	Val	Arg	515	520	525
Lys	Thr	Ile	Ser	His	Leu	Pro	Ile	Gln	Leu	Trp	Cys	Val	Glu	Arg	530	535	540
Pro	Leu	Asp	Leu	Lys	Tyr	Val	Ser	Asn	Gly	Leu	Arg	Thr	Gln	Gln	545	550	555
Asn	Ala	Ser	Ile	Asn	Met	Gln	Leu	Pro	Ser	Arg	Glu	Thr	Asn	Pro	560	565	570

Tyr Phe Asn Ser Leu Asp Gln Lys Asp Leu Val Gly Tyr Leu Ser  
 575 580 585  
 Pro Arg Ala Asn Ser Val Pro Ile Ile Pro Ser Met Gly Leu Glu  
 590 595 600  
 Glu Thr Cys Met Gln Met Pro Gly Ile Ser Asp Val Lys Ser Ile  
 605 610 615  
 Lys Trp Cys Lys Asn Ser Tyr Ser Ala Asp Ile Val Asn Ala Ser  
 620 625 630  
 Met Pro Val Ser Asp Cys Leu Leu Glu Glu Gln Gln Glu Val Lys  
 635 640 645  
 Ile Leu Leu Glu Thr Val Gln Glu Gln Ile Arg Ile Leu Thr Asp  
 650 655 660  
 Ala Arg Arg Ser Glu Asp Phe Glu Leu Ala Ser Met Glu Thr Glu  
 665 670 675  
 Asp Ser Ala Ser Glu Asn Thr Ala Phe Leu Pro Leu Ser Pro Thr  
 680 685 690  
 Ala Lys Ser Glu Arg Glu Ala Gln Phe Val Leu Arg Asn Glu Ile  
 695 700 705  
 Gln Arg Asp Ser Val Leu Thr Lys  
 710 713

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: mNRG3 extracellular domainAmino acid seq
- (B) LOCATION: 1-362
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Glu Gly Ala Ala Gly Ala Ser Pro Pro Gly Ala Ala Ser  
 1 5 10 15  
 Ala Ala Ala Ala Ser Ala Glu Glu Gly Thr Ala Ala Ala Ala Ala  
 20 25 30  
 Ala Ala Ala Ala Gly Gly Gly Pro Asp Gly Gly Gly Glu Gly Ala  
 35 40 45  
 Ala Glu Pro Pro Arg Glu Leu Arg Cys Ser Asp Cys Ile Val Trp  
 50 55 60

Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	125	130	135
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	140	145	150
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	155	160	165
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	170	175	180
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Pro	Thr	Val	Leu	Ser	185	190	195
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Pro	Gly	Ser	Arg	Pro	200	205	210
Pro	Met	Pro	Gly	Ala	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro	215	220	225
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro	230	235	240
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ala	Ala	Ser	Ser	245	250	255
Ser	Ser	Pro	Ser	Ser	Thr	Ser	Ser	Thr	Thr	Thr	Thr	Pro	Glu	Thr	260	265	270
Ser	Thr	Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	275	280	285
Ser	Glu	His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	290	295	300
Leu	Asn	Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	305	310	315
His	Lys	His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	320	325	330
Asp	Gln	Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	335	340	345

Asp His Leu Gly Ile Glu Phe Met Glu Ser Glu Asp Val Tyr Gln  
 350 355 360

Arg Gln  
 362

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 47 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: NRG3 EGF-like domain/amino acid seq.  
 (B) LOCATION: 1-47  
 (C) IDENTIFICATION METHOD:  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys Leu Asn  
 1 5 10 15  
 Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser His Lys  
 20 25 30  
 His Cys Arg Cys Lys Glu Gly Tyr Gln Gly Val Arg Cys Asp Gln  
 35 40 45  
 Phe Leu  
 47

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2502 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Human NRG3B1(hNRG3B1)/nucleic acid seq.  
 (B) LOCATION: 1-2502  
 (C) IDENTIFICATION METHOD:  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCACCGACCT AGTGGACTCC ACTAGGTCGG TGGGCACGTA CTCCTTGACG 50  
 GAGCCCACCA CGATCCATTT GAGAAGCATG AGGCGCGGCC CCATGCCTCT 100  
 GCCGCGGCCC TCGGGGGGGC GAAGGTGAAN ACCGGCTCCT AGGATGAGTG 150  
 AAGGGGCGGC CGCTGCCTCG CCACCTGGTG CCGCTTCGGC AGCCGCCGCC 200



TCGGCCGAGG AGGGCACCGC GGCGGCTGCG GCGGCGGCAG CGGCGGGCGG 250  
 GGGCCCGGAC GGCGGCGGCG AAGGGGCGGC CGAGCCCCC CGGGAGTTAC 300  
 GCTGTAGCGA CTGCATCGTG TGGAACCGGC AGCAGACGTG GCTGTGCGTG 350  
 GTACCTCTGT TCATCGGCTT CATCGGCCTG GGGCTCAGCC TCATGCTTCT 400  
 CAAATGGATC GTGGTGGGCT CCGTCAAGGA GTACGTGCCC ACCGACCTAG 450  
 TGGACTCCAA GGGGATGGGC CAGGACCCCT TCTTCCTCTC CAAGCCCAGC 500  
 TCTTTCCCCA AGGCCATGGA GACCACCACC ACTACCACTT CCACCACGTC 550  
 CCCC GCCACC CCCTCCGCCG GGGGTGCCGC CTCCTCCAGG ACGCCCAACC 600  
 GGATTAGCAC TCGCCTGACC ACCATCACGC GGGCGCCAC TCGCTTCCCC 650  
 GGGCACGGG TGCCCATCCG GGCCAGCCCG CGCTCCACCA CAGCACGGAA 700  
 CACTGCGGCC CCTGCGACGG TCCCGTCCAC CACGGCCCCG TTCTTCAGTA 750  
 GCAGCACGCT GGGCTCCCGA CCCCCGGTGC CAGGAACTCC AAGTACCCAG 800  
 GCAATGCCCT CCTGGCCTAC TGCGGCATAC GCTACCTCCT CCTACCTTCA 850  
 CGATTCTACT CCCTCCTGGA CCCTGTCTCC CTTTCAGGAT GCTGCCTCCT 900  
 CTTCTTCCTC TTCTTCCTCC TCCGCTACCA CCACCACACC AGAACTAGC 950  
 ACCAGCCCCA AATTTTCATAC GACGACATAT TCCACAGAGC GATCCGAGCA 1000  
 CTTCAAACCC TGCCGAGACA AGGACCTTGC ATACTGTCTC AATGATGGCG 1050  
 AGTGCTTTGT GATCGAAACC CTGACCGGAT CCCATAAACA CTGTCGGTGC 1100  
 AAAGAAGGCT ACCAAGGAGT CCGTTGTGAT CAATTTCTGC CGAAAACTGA 1150  
 TTCCATCTTA TCGGATCCAA CAGACCACTT GGGGATTGAA TTCATGGAGA 1200  
 GTGAAGAAGT TTATCAAAGG CAGGTGCTGT CAATTCATG TATCATCTTT 1250  
 GGAATTGTCA TCGTGGGCAT GTTCTGTGCA GCATTCTACT TCAAAAGCAA 1300  
 GAAACAAGCT AAACAAATCC AAGAGCAGCT GAAAGTGCCA CAAAATGGTA 1350  
 AAAGCTACAG TCTCAAAGCA TCCAGCACAA TGGCAAAGTC AGAGAACTTG 1400  
 GTGAAGAGCC ATGTCCAGCT GCAAAATTAT TCAAAGGTGG AAAGGCATCC 1450  
 TGTGACTGCA TTGGAGAAAA TGATGGAGTC AAGTTTGTG GGGCCCCAGT 1500  
 CATTCCTGA GGTCCCTTCT CCTGACAGAG GAAGCCAGTC TGTCAAACAC 1550  
 CACAGGAGTC TATCCTCTTG CTGCAGCCCA GGGCAAAGAA GTGGCATGCT 1600  
 CCATAGGAAT GCCTTCAGAA GGACACCCCC GTCACCCCGA AGTAGGCTAG 1650

GTGGAATTGT GGGACCAGCA TATCAGCAAC TCGAAGAATC AAGGATCCCA 1700  
 GACCAGGATA CGATACCTTG CCAAGGGATA GAGGTCAGGA AGACTATATC 1750  
 CCACCTGCCT ATACAGCTGT GGTGTGTTGA AAGACCCCTG GACTTAAAGT 1800  
 ATTCATCCAG TGGTTTAAAA ACCCAACGAA ATACATCAAT AAATATGCAA 1850  
 CTGCCTTCAA GAGAGACAAA CCCCTATTTT AATAGCTTGG AGCAAAAGGA 1900  
 CCTGGTGGGC TATTCATCCA CAAGGGCCAG TTCTGTGCCC ATCATCCCTT 1950  
 CAGTGGGTTT AGAGGAAACC TGCCTGCAAA TGCCAGGGAT TTCTGAAGTC 2000  
 AAAAGCATCA AATGGTGCAA AAACCTCTAT TCAGCTGACG TTGTCAATGT 2050  
 GAGTATTCCA GTCAGCGATT GTCTTATAGC AGAACAACAA GAAGTGAAAA 2100  
 TATTGCTAGA AACTGTCCAG GAGCAGATCC GAATTCTGAC TGATGCCAGA 2150  
 CGGTCAGAAG ACTACGAACT GGCCAGCGTA GAAACCGAGG ACAGTGCAAG 2200  
 CGAAAACACA GCCTTTCTCC CCCTGAGTCC CACAGCCAAA TCAGAACGAG 2250  
 AGGCGCAATT TGTCTTAAGA AATGAAATAC AAAGAGACTC TGCATTGACC 2300  
 AAGTGACTTG AGATGTAGGA ATCTGTGCAT TCTATGCTTT GCTCAACAGG 2350  
 AAAGAGAGGA AATCAAATAC AAATTATTTA TATGCATTAA TTTAAGAGCA 2400  
 TCTACTTAGA AGAAACCAAA TAGTCTATCG CCCTCATATC ATAGTGTTTT 2450  
 TTAACAAAAT ATTTTTTTAA GGGAAAGAAA TGTTTCAGGA GGGATAAAGC 2500  
 TT 2502

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3B1 amino acid sequence
- (B) LOCATION: 1-720
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser
1				5					10					15
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala
				20					25					30

Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	
				35					40					45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	
				50					55					60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	
				65					70					75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	
				80					85					90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	
				95					100					105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	
				110					115					120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	
				125					130					135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	
				140					145					150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	
				155					160					165	
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	
				170					175					180	
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser	
				185					190					195	
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro	
				200					205					210	
Pro	Val	Pro	Gly	Thr	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro	
				215					220					225	
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro	
				230					235					240	
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ser	Ser	Ser	Ser	
				245					250					255	
Ser	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Thr	Thr	Pro	Glu	Thr	Ser	Thr	
				260					265					270	
Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	Ser	Glu	
				275					280					285	
His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	Leu	Asn	
				290					295					300	
Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	His	Lys	
				305					310					315	



Ile	Pro	Ser	Val	Gly	Leu	Glu	Glu	Thr	Cys	Leu	Gln	Met	Pro	Gly	605	610	615
Ile	Ser	Glu	Val	Lys	Ser	Ile	Lys	Trp	Cys	Lys	Asn	Ser	Tyr	Ser	620	625	630
Ala	Asp	Val	Val	Asn	Val	Ser	Ile	Pro	Val	Ser	Asp	Cys	Leu	Ile	635	640	645
Ala	Glu	Gln	Gln	Glu	Val	Lys	Ile	Leu	Leu	Glu	Thr	Val	Gln	Glu	650	655	660
Gln	Ile	Arg	Ile	Leu	Thr	Asp	Ala	Arg	Arg	Ser	Glu	Asp	Tyr	Glu	665	670	675
Leu	Ala	Ser	Val	Glu	Thr	Glu	Asp	Ser	Ala	Ser	Glu	Asn	Thr	Ala	680	685	690
Phe	Leu	Pro	Leu	Ser	Pro	Thr	Ala	Lys	Ser	Glu	Arg	Glu	Ala	Gln	695	700	705
Phe	Val	Leu	Arg	Asn	Glu	Ile	Gln	Arg	Asp	Ser	Ala	Leu	Thr	Lys	710	715	720

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3 extracellular domain/Amino AcidSeq
- (B) LOCATION: 1-360
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	1	5	10	15
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90	

Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser		95	100	105
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser		110	115	120
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr		125	130	135
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr		140	145	150
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro		155	160	165
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg		170	175	180
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser		185	190	195
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro		200	205	210
Pro	Val	Pro	Gly	Thr	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro		215	220	225
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro		230	235	240
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ser	Ser	Ser	Ser		245	250	255
Ser	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Thr	Thr	Pro	Glu	Thr	Ser	Thr		260	265	270
Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	Ser	Glu		275	280	285
His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	Leu	Asn		290	295	300
Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	His	Lys		305	310	315
His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	Asp	Gln		320	325	330
Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	Asp	His		335	340	345
Leu	Gly	Ile	Glu	Phe	Met	Glu	Ser	Glu	Glu	Val	Tyr	Gln	Arg	Gln		350	355	360

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: NRG3 EGF-like domain/amino acid seq.
- (B) LOCATION: 1-47
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys Leu Asn  
1 5 10 15  
Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser His Lys  
20 25 30  
His Cys Arg Cys Lys Glu Gly Tyr Gln Gly Val Arg Cys Asp Gln  
35 40 45  
Phe Leu  
47

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: cARIA.egf
- (B) LOCATION: 1-48
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

His Leu Thr Lys Cys Asp Ile Lys Gln Lys Ala Phe Cys Val Asn  
1 5 10 15  
Gly Gly Glu Cys Tyr Met Val Lys Asp Leu Pro Asn Pro Pro Arg  
20 25 30  
Tyr Leu Cys Arg Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln  
35 40 45  
Asn Tyr Val  
48

[illegible]

(A) LENGTH: 45 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(A) NAME/KEY: hAR.egf  
(B) LOCATION: 1-45  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

Lys	Lys	Asn	Pro	Cys	Asn	Ala	Glu	Phe	Gln	Asn	Phe	Cys	Ile	His
1				5					10					15
Gly	Glu	Cys	Lys	Tyr	Ile	Glu	His	Leu	Glu	Ala	Val	Thr	Cys	Lys
				20					25					30
Cys	Gln	Gln	Glu	Tyr	Phe	Gly	Glu	Arg	Cys	Gly	Glu	Lys	Ser	Met
				35					40					45

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(A) NAME/KEY: hBTC.efg  
(B) LOCATION: 1-45  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

His	Phe	Ser	Arg	Cys	Pro	Lys	Gln	Tyr	Lys	His	Tyr	Cys	Ile	Lys
1				5					10					15
Gly	Arg	Cys	Arg	Phe	Val	Val	Ala	Glu	Gln	Thr	Pro	Ser	Cys	Val
				20					25					30
Cys	Asp	Glu	Gly	Tyr	Ile	Gly	Ala	Arg	Cys	Glu	Arg	Val	Asp	Leu
				35					40					45

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(A) NAME/KEY: hEGF.egf  
(B) LOCATION: 1-46



(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His  
1 5 10 15  
Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys  
20 25 30  
Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp  
35 40 45  
Leu  
46

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(ix) FEATURE:

(A) NAME/KEY: hHB-EGF.egf  
(B) LOCATION: 1-45  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His  
1 5 10 15  
Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys Ile  
20 25 30  
Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu  
35 40 45

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(ix) FEATURE:

(A) NAME/KEY: hHRGalpha.egf  
(B) LOCATION: 1-49  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
1 5 10 15

Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg  
20 25 30  
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr  
35 40 45  
Glu Asn Tyr Pro  
49

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hHRGbeta.egf  
(B) LOCATION: 1-48  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
1 5 10 15  
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg  
20 25 30  
Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln  
35 40 45  
Asn Tyr Val  
48

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hTGFalpha.egf  
(B) LOCATION: 1-45  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

His Phe Asn Asp Cys Pro Asp Ser His Thr Gln Phe Cys Phe His  
1 5 10 15  
Gly Thr Cys Arg Phe Leu Val Gln Glu Asp Lys Pro Ala Cys Val  
20 25 30



**THE UNIVERSITY OF CHICAGO**

(A) LENGTH: 8 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(A) NAME/KEY: hNRG3B1 transmembrane proximal 1  
(B) LOCATION: 1-8  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

Asn Asp Gly Glu Cys Phe Val Ile  
1 5 8

(A) LENGTH: 9 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(A) NAME/KEY: hNRG3B1 transmembrane proximal 2  
(B) LOCATION: 1-9  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

Glu Phe Met Glu Ser Glu Glu Val Tyr  
1 5 9

(A) LENGTH: 466 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(A) NAME/KEY: EST Genbank entry H23651  
(B) LOCATION: 1-466  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

AATTTCTGCC	GAAAACTGAT	TCCATCTTAT	CGGATCCAAC	AGACCACTTG	50
GGGATTGAAT	TCATGGAGAG	TGAAGAAGTT	TATCAAAGGC	AGGTGCTGTC	100
AATTTTCATGT	ATCATCTTTG	GAATTGTCAT	CGTGGGCATG	TTCTGTGCAG	150

CATTCTACTT CAAAAGCAAG AAACAAGCTA AACAAATCCA AGAGCAGCTG 200  
AAAGTGCCAC AAAATGGTAA AAGCTACAGT CTCAAAGCAT CCAGCACAAT 250  
GGCAAAGTCA GAGAACTTGG TGAAGAGCCA TGTCCAGCTG CAAAATAAAA 300  
TGTCAGGCTT CTGAGCCCAA GCTAAGCCAT CATATCCCCT GTNGACCTGC 350  
ACGTGCACAT CCNGATGGCC CGTTTCCTGC CTTTTNTGAT GACATTNCA 400  
CCACAAATGN AGTGAAAATG GGNCTTTTCN TGCCTTAACT GGTGACNTT 450  
TTTNCCCCAA AAGGAG 466

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2091 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Human NRG3B2 (hNRGB2)
- (B) LOCATION: 1-2091
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGAGTGAAG GGGCGGCCGC TGCCTCGCCA CCTGGTGCCG CTTCGGCAGC 50  
CGCCGCTCG GCCGAGGAGG GCACCGCGGC GGCTGCGGCG GCGGCAGCGG 100  
CGGGCGGGGG CCCGGACGGC GCGGGCGAAG GGGCGGCCGA GGGGGGGGG 150  
GAGTTACGCT GTAGCGACTG CATCGTGTGG AACCGGCAGC AGACGTGGCT 200  
GTGCGTGGTA CCTCTGTTCA TCGGCTTCAT CGGCCTGGGG CTCAGCCTCA 250  
TGCTTCTCAA ATGGATCGTG GTGGGCTCCG TCAAGGAGTA CGTGCCCAACC 300  
GACCTAGTGG ACTCCAAGGG GATGGGCCAG GACCCCTTCT TCCTCTCCAA 350  
GCCCAGCTCT TTCCCAAGG CCATGGAGAC CACCACCACT ACCACTTCCA 400  
CCACGTCCCC CGCCACCCCC TCCGCCGGGG GTGCCGCCTC CTCCAGGACG 450  
CCCAACCGGA TTAGCACTCG CCTGACCACC ATCACGCGGG CGCCCACTCG 500  
CTTCCCCGGG CACCGGGTGC CCATCCGGGC CAGCCCGCGC TCCACCACAG 550  
CACGGAACAC TGCGGGCCCT GCGACGGTCC CGTCCACCAC GGCCCCGTTC 600  
TTCAGTAGCA GCACGCTGGG CTCCCGACCC CCGGTGCCAG GAACTCCAAG 650  
TACCCAGGCA ATGCCCTCCT GGCCTACTGC GGCATACGCT ACCTCCTCCT 700

ACCTTCACGA	TTCTACTCCC	TCCTGGACCC	TGTCTCCCTT	TCAGGATGCT	750
GCCTCCTCTT	CTTCCTCTTC	TTCCTCCTCC	GCTACCACCA	CCACACCAGA	800
AACTAGCACC	AGCCCCAAAT	TTCATACGAC	GACATATTCC	ACAGAGCGAT	850
CCGAGCACTT	CAAACCCTGC	CGAGACAAGG	ACCTTGCATA	CTGTCTCAAT	900
GATGGCGAGT	GCTTTGTGAT	CGAAACCCTG	ACCGGATCCC	ATAAACACTG	950
TCGGTGCAAA	GAAGGCTACC	AAGGAGTCCG	TTGTGATCAA	TTTCTGCCGA	1000
AAACTGATTC	CATCTTATCG	GATCCAACAG	ACCACTTGGG	GATTGAATTC	1050
ATGGAGAGTG	AAGAAGTTTA	TCAAAGGCAG	GTGCTGTCAA	TTTCATGTAT	1100
CATCTTTGGA	ATTGTCATCG	TGGGCATGTT	CTGTGCAGCA	TTCTACTTCA	1150
AAAGCAAGAA	ACAAGCTAAA	CAAATCCAAG	AGCAGCTGAA	AGTGCCACAA	1200
AATGGTAAAA	GCTACAGTCT	CAAAGCATCC	AGCACAATGG	CAAAGTCAGA	1250
GAACTTGGTG	AAGAGCCATG	TCCAGCTGCA	AAATTATTCA	AAGGTGGAAA	1300
GGCATCCTGT	GACTGCATTG	GAGAAAATGA	TGGAGTCAAG	TTTTGTCCGC	1350
CCCCAGTCAT	TCCCTGAGGT	CCCTTCTCCT	GACAGAGGAA	GCCAGTCTGT	1400
CAAACACCAC	AGGAGTCTAT	CCTCTTGCTG	CAGCCCAGGG	CAAAGAAGTG	1450
GCATGCTCCA	TAGGAATGCC	TTCAGAAGGA	CACCCCCGTC	ACCCCGAAGT	1500
AGGCTAGGTG	GAATTGTGGG	ACCAGCATAT	CAGCAACTCG	AAGAATCAAG	1550
GATCCCAGAC	CAGGATACGA	TACCTTGCCA	AGGGTATTCA	TCCAGTGGTT	1600
TAAAAACCCA	ACGAAATACA	TCAATAAATA	TGCAACTGCC	TTCAAGAGAG	1650
ACAAACCCCT	ATTTTAATAG	CTTGGAGCAA	AAGGACCTGG	TGGGCTATTC	1700
ATCCACAAGG	GCCAGTTCTG	TGCCCATCAT	CCCTTCAGTG	GGTTTAGAGG	1750
AAACCTGCCT	GCAAATGCCA	GGGATTTCTG	AAGTCAAAAG	CATCAAATGG	1800
TGCAAAAAC	CCTATTGAGC	TGACGTTGTC	AATGTGAGTA	TTCCAGTCAG	1850
CGATTGTCTT	ATAGCAGAAC	AACAAGAAGT	GAAATATTG	CTAGAAACTG	1900
TCCAGGAGCA	GATCCGAATT	CTGACTGATG	CCAGACGGTC	AGAAGACTAC	1950
GAAGTGGCCA	GCGTAGAAAC	CGAGGACAGT	GCAAGTGAAA	ACACAGCCTT	2000
TCTCCCCCTG	AGTCCCACAG	CCAAATCAGA	ACGAGAGGCG	CAATTTGTCT	2050
TAAGAAATGA	AATACAAAGA	GACTCTGCAT	TGACCAAGTG	A	2091

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Human NRG3B2
- (B) LOCATION: 1-696
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	
1				5					10					15	
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	
				20					25					30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	
				35					40					45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	
				50					55					60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	
				65					70					75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	
				80					85					90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	
				95					100					105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	
				110					115					120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	
				125					130					135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	
				140					145					150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	
				155					160					165	
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	
				170					175					180	
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser	
				185					190					195	
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro	
				200					205					210	

Pro	Val	Pro	Gly	Thr	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro
				215					220					225
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro
				230					235					240
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ser	Ser	Ser	Ser
				245					250					255
Ser	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Thr	Thr	Pro	Glu	Thr	Ser	Thr
				260					265					270
Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	Ser	Glu
				275					280					285
His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	Leu	Asn
				290					295					300
Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	His	Lys
				305					310					315
His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	Asp	Gln
				320					325					330
Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	Asp	His
				335					340					345
Leu	Gly	Ile	Glu	Phe	Met	Glu	Ser	Glu	Glu	Val	Tyr	Gln	Arg	Gln
				350					355					360
Val	Leu	Ser	Ile	Ser	Cys	Ile	Ile	Phe	Gly	Ile	Val	Ile	Val	Gly
				365					370					375
Met	Phe	Cys	Ala	Ala	Phe	Tyr	Phe	Lys	Ser	Lys	Lys	Gln	Ala	Lys
				380					385					390
Gln	Ile	Gln	Glu	Gln	Leu	Lys	Val	Pro	Gln	Asn	Gly	Lys	Ser	Tyr
				395					400					405
Ser	Leu	Lys	Ala	Ser	Ser	Thr	Met	Ala	Lys	Ser	Glu	Asn	Leu	Val
				410					415					420
Lys	Ser	His	Val	Gln	Leu	Gln	Asn	Tyr	Ser	Lys	Val	Glu	Arg	His
				425					430					435
Pro	Val	Thr	Ala	Leu	Glu	Lys	Met	Met	Glu	Ser	Ser	Phe	Val	Gly
				440					445					450
Pro	Gln	Ser	Phe	Pro	Glu	Val	Pro	Ser	Pro	Asp	Arg	Gly	Ser	Gln
				455					460					465
Ser	Val	Lys	His	His	Arg	Ser	Leu	Ser	Ser	Cys	Cys	Ser	Pro	Gly
				470					475					480
Gln	Arg	Ser	Gly	Met	Leu	His	Arg	Asn	Ala	Phe	Arg	Arg	Thr	Pro
				485					490					495



Pro Ser Pro Arg Ser Arg Leu Gly Gly Ile Val Gly Pro Ala Tyr  
 500 505 510  
 Gln Gln Leu Glu Glu Ser Arg Ile Pro Asp Gln Asp Thr Ile Pro  
 515 520 525  
 Cys Gln Gly Tyr Ser Ser Ser Gly Leu Lys Thr Gln Arg Asn Thr  
 530 535 540  
 Ser Ile Asn Met Gln Leu Pro Ser Arg Glu Thr Asn Pro Tyr Phe  
 545 550 555  
 Asn Ser Leu Glu Gln Lys Asp Leu Val Gly Tyr Ser Ser Thr Arg  
 560 565 570  
 Ala Ser Ser Val Pro Ile Ile Pro Ser Val Gly Leu Glu Glu Thr  
 575 580 585  
 Cys Leu Gln Met Pro Gly Ile Ser Glu Val Lys Ser Ile Lys Trp  
 590 595 600  
 Cys Lys Asn Ser Tyr Ser Ala Asp Val Val Asn Val Ser Ile Pro  
 605 610 615  
 Val Ser Asp Cys Leu Ile Ala Glu Gln Gln Glu Val Lys Ile Leu  
 620 625 630  
 Leu Glu Thr Val Gln Glu Gln Ile Arg Ile Leu Thr Asp Ala Arg  
 635 640 645  
 Arg Ser Glu Asp Tyr Glu Leu Ala Ser Val Glu Thr Glu Asp Ser  
 650 655 660  
 Ala Ser Glu Asn Thr Ala Phe Leu Pro Leu Ser Pro Thr Ala Lys  
 665 670 675  
 Ser Glu Arg Glu Ala Gln Phe Val Leu Arg Asn Glu Ile Gln Arg  
 680 685 690  
 Asp Ser Ala Leu Thr Lys  
 695 696